

PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/509,796

DATE: 10/08/2004 TIME: 12:01:03

Input Set : A:\PTO.FG.txt Output Set: N:\CRF4\10082004\J509796.raw

5 <110> APPLICANT: BASF Plant Science GmbH 7 <120> TITLE OF INVENTION: Expression of Phospholipids:Diacylqlycerine Acyltransferase (PDAT) for

the Production of Plant Storage Lipids with Polyunsaturated Fatty Acids 8

9 <130> FILE REFERENCE: 1

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/509,796

C--> 10 <141> CURRENT FILING DATE: 2004-09-29

W--> 10 <160> NUMBER OF SEQ ID: 2

11 <170> SOFTWARE: PatentIn version 3.1

W--> 12 <210> SEQ ID NO: 1

13 <211> LENGTH: 2425

14 <212> TYPE: DNA

15 <213> ORGANISM: Physcomitrella patens

17 <220> FEATURE:

19 <221> NAME/KEY: CDS

21 <222> LOCATION: (120)..(2135)

23 <223> OTHER INFORMATION: Phospholipid:Diacylqlycerin-Acyltransferase 26 <400> SEQUENCE: 1 27 agaaacaget etttgtetet etegaetgat etaacaatee etaatetgtg ttetaaatte 60 29 ctggacgaga tttgacaaag tccgtatagc ttaacctggt ttaatttcaa gtgacagat 119 31 atg ccc ctt att cat cgg aaa aag ccg acg gag aaa cca tcg acg ccg 167 32 Met Pro Leu Ile His Arg Lys Lys Pro Thr Glu Lys Pro Ser Thr Pro 33 1 35 cca tct gaa gag gtg gtg cac gat gag gat tcg caa aag aaa cca cac 215 36 Pro Ser Glu Glu Val Val His Asp Glu Asp Ser Gln Lys Lys Pro His 20 25 39 gaa tot too aaa too cac cat aag aaa tog aac gga gga ggg aag tgg 263 40 Glu Ser Ser Lys Ser His His Lys Lys Ser Asn Gly Gly Lys Trp 40 43 tcg tgc atc gat tct tgt tgt tgg ttc att ggg tgt gtg tgt gta acc 311 44 Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr 45 55 47 tgg tgg ttt ctt ctc ttc ctt tac aac gca atg cct gcg agc ttc cct 359 48 Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro 407 51 cag tat gta acg gag cga atc acg ggt cct ttg cct gac ccg ccc.ggt 52 Gln Tyr Val Thr Glu Arg Ile Thr Gly Pro Leu Pro Asp Pro Pro Gly 55 gtt aag ctc aaa aaa gaa ggt ctt aag gcg aaa cat cct gtt gtc ttc 455 56 Val Lys Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe 105

59 att cct ggg att gtc acc ggt ggg ctc gag ctt tgg gaa ggc aaa caa

60 Ile Pro Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln

120



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503

115

61



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63 tgc gct gat ggt tta ttt aga aaa cgt ttg tgg ggt gga act ttt ggt 64 Cys Ala Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Gly 65 130 135 140	551
67 gaa gtc tac aaa agg cct cta tgt tgg gtg gaa cac atg tca ctt gac 68 Glu Val Tyr Lys Arg Pro Leu Cys Trp Val Glu His Met Ser Leu Asp 69 145 150 155 160	599
71 aat gaa act ggg ttg gat cca gct ggt att aga gtt cga gct gta tca 72 Asn Glu Thr Gly Leu Asp Pro Ala Gly Ile Arg Val Arg Ala Val Ser 73 165 170 175	647
75 gga ctc gtg gct gct gac tac ttt gct cct ggc tac ttt gtc tgg gca 76 Gly Leu Val Ala Ala Asp Tyr Phe Ala Pro Gly Tyr Phe Val Trp Ala 77 180 185 190	695
79 gtg ctg att gct aac ctt gca cat att gga tat gaa gag aaa aat atg 80 Val Leu Ile Ala Asn Leu Ala His Ile Gly Tyr Glu Glu Lys Asn Met 81 195 200 205	743
83 tac atg gct gca tat gac tgg cgg ctt tcg ttt cag aac aca gag gta 84 Tyr Met Ala Ala Tyr Asp Trp Arg Leu Ser Phe Gln Asn Thr Glu Val 85 210 215 220	791
87 cgt gat cag act ctt agc cgt atg aaa agt aat ata gag ttg atg gtt 88 Arg Asp Gln Thr Leu Ser Arg Met Lys Ser Asn Ile Glu Leu Met Val 89 225 230 235 240	839
91 tct acc aac ggt gga aaa aaa gca gtt ata gtt ccg cat tcc atg ggg 92 Ser Thr Asn Gly Gly Lys Lys Ala Val Ile Val Pro His Ser Met Gly 93 245 250 255	887
95 gtc ttg tat ttt cta cat ttt atg aag tgg gtt gag gca cca gct cct 96 Val Leu Tyr Phe Leu His Phe Met Lys Trp Val Glu Ala Pro Ala Pro 97 260 265 270	935
99 ctg ggt ggc ggg ggt ggg cca gat tgg tgt gca aag tat att aag gcg 100 Leu Gly Gly Gly Gly Pro Asp Trp Cys Ala Lys Tyr Ile Lys Ala 101 275 280 285	983
103 gtg atg aac att ggt gga cca ttt ctt ggt gtt cca aaa gct gtt gca 104 Val Met Asn Ile Gly Gly Pro Phe Leu Gly Val Pro Lys Ala Val Ala 105 290 295 300	1031
107 ggg ctt ttc tct gct gaa gca aag gat gtt gca gtt gcc aga gcg att 108 Gly Leu Phe Ser Ala Glu Ala Lys Asp Val Ala Val Ala Arg Ala Ile 109 305 310 315 320	1079
108 Gly Leu Phe Ser Ala Glu Ala Lys Asp Val Ala Val Ala Arg Ala Ile 109 305 310 315 320 111 gcc cca gga ttc tta gac acc gat ata ttt aga ctt cag acc ttg cag 112 Ala Pro Gly Phe Leu Asp Thr Asp Ile Phe Arg Leu Gln Thr Leu Gln 113 325 330 335	1127
108 Gly Leu Phe Ser Ala Glu Ala Lys Asp Val Ala Val Ala Arg Ala Ile 109 305 310 315 320 111 gcc cca gga ttc tta gac acc gat ata ttt aga ctt cag acc ttg cag 112 Ala Pro Gly Phe Leu Asp Thr Asp Ile Phe Arg Leu Gln Thr Leu Gln 113 325 330 335 115 cat gta atg aga atg aca cgc aca tgg gac tca aca atg tct atg 116 His Val Met Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu 117 340 345 350	1127 1175
108 Gly Leu Phe Ser Ala Glu Ala Lys Asp Val Ala Val Ala Arg Ala Ile 109 305 310 315 320 111 gcc cca gga ttc tta gac acc gat ata ttt aga ctt cag acc ttg cag 112 Ala Pro Gly Phe Leu Asp Thr Asp Ile Phe Arg Leu Gln Thr Leu Gln 113 325 330 335 115 cat gta atg aga atg aca cgc aca tgg gac tca aca atg tct atg tta 116 His Val Met Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu	1127
108 Gly Leu Phe Ser Ala Glu Ala Lys Asp Val Ala Val Ala Arg Ala Ile 109 305 310 315 320 111 gcc cca gga ttc tta gac acc gat ata ttt aga ctt cag acc ttg cag 112 Ala Pro Gly Phe Leu Asp Thr Asp Ile Phe Arg Leu Gln Thr Leu Gln 113 325 330 335 115 cat gta atg aga atg aca cgc aca tgg gac tca aca atg tct atg tta 116 His Val Met Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu 117 340 345 350 119 ccg aag gga ggt gac acg ata tgg ggc ggg ctt gat tgg tca ccg gag 120 Pro Lys Gly Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu	1127 1175

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128 129	_	Glu	Ala	Gly	Glu	Asn 390	Gly	Val	Ser	Lys	Lys 395	Ser	Pro	Val	Asn	Tyr 400	
		agg	ato	ata	tct	ttt	aaa	aaa	gaa	gta	gca	gag	act.	aca	cca	tct	1367
						Phe											
	GIY	Arg	riec	116		rne	GLY	цуз	GIU	410	niu	Olu	711u	2114	415	DCI	
133					405												1415
						gat											1415
136	Glu	Ile	Asn		Ile	Asp	Phe	Arg	_	Ala	Val	Lys	GIY		Ser	TIE	
137				420					425					430			
						cgt											1463
140	Pro	Asn	His	Thr	Cys	Arg	Asp	Val	\mathtt{Trp}	Thr	Glu	Tyr	His	Asp	Met	Gly	
141			435					440					445				
143	att	gct	ggg	atc	aaa	gct	atc	gct	gag	tat	aag	gtc	tac	act	gct	ggt	1511
144	Ile	Ala	Gly	Ile	Lys	Ala	Ile	Ala	Glu	Tyr	Lys	Val	Tyr	Thr	Ala	Gly	
145		450	_		_		455					460					
147	qaa	qct	ata	gat	cta	cta	cat	tat	qtt	qct	cct	aaq	atg	atg	gcg	cgt	1559
						Leu											
149						470		- 4 -			475	-				480	
		acc	act	cat	ttc	tct	tat	gga	att	act		gat	t.t.a	gat.	gac	acc	1607
						Ser											
153	Gry	AIG	AΙα	1115	485		- 7 -	O J		490	1105	110p		1101	495		
	226	+ - +	a aa	ant.		aaa	+ 20	taa	+ ==		cca	++=	asa	202		tta	1655
						Lys											1000
	ьуѕ	TAT	GIII		PIO	пур	TAT	пр		ASII	PIO	пеп	GIU	510	пур	пец	
157		4.		500					505			+	~~~		~~~	2+2	1703
						atg											1703
	Pro	Asn		Pro	GIU	Met	GIU			ser	ьeu	туг		var	GIY	iie	
161			515					520					525				1051
						tac											1751
	Pro		Glu	Arg	Ala	Tyr		Tyr	Lys	Leu	Asn		ser	Pro	Asp	ser	
165		530					535					540					
						ata											1799
168	Cys	Ile	Pro	Phe	Gln	Ile	Phe	Thr	Ser	Ala	His	Glu	Glu	Asp	Glu		
169	545					550					555					560	
						gga											1847
172	Ser	Cys	Leu	Lys	Ala	Gly	Val	Tyr	Asn	Val	Asp	Gly	Asp	Glu	Thr	Val	
173					565					570					575		
175	CCC	gtc	cta	agt	gcc	ggg	tac	atg	tgt	gca	aaa	gcg	tgg	cgt	ggc	aag	1895
176	Pro	Val	Leu	Ser	Ala	Gly	Tyr	Met	Cys	Ala	Lys	Ala	Trp	Arg	Gly	Lys	
177				580		_	_		585					590			
179	aca	aqa	ttc	aac	cct	tcc	qqa	atc	aaq	act	tat	ata	aga	gaa	tac	aat	1943
		_				Ser											
181			595				-	600	-		•		605		•		
	cac	tct		cċa	act	aac	cta		gaa	aga	cac	aaa	acq	caq	agt	aat	1991
						Asn											
185	*****	610		110	2124		615			0 -1		620				- 1	
	aaa		at+	ast	ato	atg		220	+++	act	tta		gaa	gat	atc	atα	2039
						Met											2000
	625	птв	vai	тар	116	630	GIY	UOII	FIIC	TIG	635	110	01 u	woh		640	
					~~~			~~~	+~+	~~+		~~~	as+	~~~	a		2007
						ggt											2087
192	arg	vaı	Ата	Ата	GTĀ	Gly	Asn	GTĀ	ser	Asp	тте	GTÀ	H1S	Asp	GIN	vdl	

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193					645					650					655			
195	cac	tct	ggc	ata	ttt	gaa	tgg	tcg	gag	cgt	att	gac	ctg	aag	ctg	tga	21	L35
									Glu									
197			_	660			_		665	-				670				
199	atat	cate	gat d	ctctt	taaç	ge to	tcct	gtca	gct	tate	gtga	atco	caata	act t	tgaa	aagaga	23	195
		_	-		_		-	_	_							agcctg	22	255
	_						_				-					gtaaat	23	315
	_	_														tgtttg	23	375
									a aaa						•			125
			EQ II			•	, ,,,,,											
			- ENGTI															
			YPE:															
216	<213	3> OF	RGAN	ISM:	Phys	scom:	itrel	lla r	pater	ıs								
			EQUE		_			•	•									
						Ara	Lvs	Lys	Pro	Thr	Glu	Lys	Pro	Ser	Thr	Pro	•	
222					5		-	•		10		•			15			
		Ser	Glu	Glu	Val	Val	His	qaA	Glu	qaA	Ser	Gln	Lys	Lys	Pro	His		
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	Glu	Ser	Ser		Ser	His	His	Lvs	Lys	Ser	Asn	Gly	Gly	Gly	Lys	Trp		
228			35					40	-			•	45	•	•	-		
	Ser	Cvs	Ile	qaA	Ser	Cys	Cys	Trp	Phe	Ile	Gly	Cys	Val	Cys	Val	Thr		
231		50		-		•	55	•			-	60		•				
	Trp	Trp	Phe	Leu	Leu	Phe	Leu	Tyr	Asn	Ala	Met.	Pro	Ala	Ser	Phe	Pro		
234	_	-				70		•			75					80		
236	Gln	Tyr	Val	Thr	Glu	Arg	Ile	Thr	Gly	Pro	Leu	Pro	Asp	Pro	Pro	Gly		•
237		-			85				•	90			_		95	-		
239	Val	Lys	Leu	Lys	Lys	Glu	Gly	Leu	Lys	Ala	Lys	His	Pro	Val	Val	Phe		
240		•		100	•		•		105		-			110				
243	Ile	Pro	Gly	Ile	Val	Thr	Gly	Gly	Leu	Glu	Leu	Trp	Glu	Gly	Lys	Gln		
244			115				_	120					125					
246	Cys	Ala	Asp	Gly	Leu	Phe	Arg	Lys	Arg	Leu	Trp	Gly	Gly	Thr	Phe	Gly		
247	-	130	-	-			135	-				140						
249	Glu	Val	Tyr	Lys	Arg	Pro	Leu	Cys	Trp	Val	Glu	His	Met	Ser	Leu	Asp		
250			-	_		150		_			155					160		•
253	Asn	Glu	Thr	Gly	Leu	Asp	Pro	Ala	Gly	Ile	Arg	Val	Arg	Ala	Val	Ser		
254				_	165	_			_	170					175			
256	Gly	Leu	Val	Ala	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Tyr	Phe	Val	Trp	Ala		
257	_			·180			_		185					190				
259	Val	Leu	Ile	Ala	Asn	Leu	Ala	His	Ile	Gly	Tyr	Glu	Glu	Lys	Asn	Met		
260			195					200					205					
	Tyr	Met	Ala	Ala	Tyr	Asp	Trp	Arg	Leu	Ser	Phe	Gln	Asn	Thr	Glu	Val		
263	Ī	210			_	_	215	_				220						
265	Arq	Asp	Gln	Thr	Leu	Ser	Arg	Met	Lys	Ser	Asn	Ile	Glu	Leu	Met	Val		
266		_				230	_		-		235					240		
		Thr	Asn	Gly	Gly		Lys	Ala	Val	Ile	Val	Pro	His	Ser	Met	Gly		
269				. •	245	-	-			250					255	-		
	Val	Leu	Tyr	Phe		His	Phe	Met	Lys	Trp	Val	Glu	Ala	Pro	Ala	Pro		
272			-	260					265	-				270				
	Leu	Gly	Gly	Gly	Gly	Gly	Pro	qaA	Trp	Cys	Ala	Lys	Tyr	Ile	Lys	Ala		
		-	-	-	-	-		-	-	-		-	-		-			

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275			275					280					285			
278	Val	Met	Asn	Ile	Gly	Gly	Pro	Phe	Leu	Gly	Val	Pro	Lys	Ala	Val	Ala
279		290					295					300				
281	Gly	Leu	Phe	Ser	Ala	Glu	Ala	Lys	Asp	Val	Ala	Val	Ala	Arg	Ala	Ile
282	305					310		_			315					320
		Pro	Glv	Phe	Leu	Asp	Thr	Asp	Ile	Phe	Arq	Leu	Gln	Thr	Leu	Gln
285			<b>0</b> -1		325					330					335	
	Hic	Val	Met	Ara		Thr	Ara	Thr	Trn		Ser	Thr	Met	Ser		Leu
288	1113	Vai	ricc	340	1100		9		345	p	001			350		
	Desc	T	~1		7 00	The se	т1.	Tres		C1.,	T 011	7 cn	Trn	Ser	Dro	Glu
	PIO	пур		GIY	Asp	TIIT	TIE	360	Gry	Gry	пец	Asp	365	Ser	FIO	GIU
291	<b>-</b>	<b>a</b> 1	355	ml	<b>G</b>	<b>G</b>	<b>~1</b>		T	<b>~1</b> -	T	7		<b>~1</b>	mb ~	C
			HIS	THE	Cys	Cys		гуѕ	гуя	GIII	гуя		ASII	Glu	TIIL	Cys
294		370				_	375		_	_		380			•	m
	_	Glu	Ala	GIA	GIu		GIĀ	vaı	Ser	гуѕ			Pro	Val	Asn	
	385					390	_			_	395				_	400
299	Gly	Arg	Met	Ile	Ser	Phe	Gly	Lys	Glu	Val	Ala	Glu	Ala	Ala		Ser
300					405					410					415	
302	Glu	Ile	Asn	Asn	Ile	Asp	Phe	Arg	Gly	Ala	Val	Lys	Gly	Gln	Ser	Ile
303				420					425					430		
305	Pro	Asn	His	Thr	Cys	Arg	Asp	Val	Trp	Thr	Glu	Tyr	His	Asp	Met	Gly
306			435					440					445			
308	Ile	Ala	Gly	Ile	Lys	Ala	Ile	Ala	Glu	Tyr	Lys	Val	Tyr	Thr	Ala	Gly
309		450	_		_		455					460				
311	Glu	Ala	Ile	Asp	Leu	Leu	His	Tyr	Val	Ala	Pro	Lys	Met	Met	Ala	Arg
	465			•		470		-			475	•				480
		Ala	Ala	His	Phe		Tvr	Glv	Ile	Ala	Asp	Asp	Leu	Asp	asa	Thr
315	1				485		-1-	1		490				-	495	
	Lvs	Tur	Gln	Asp		Lvs	Tvr	Trn	Ser	-	Pro	Len	Glu	Thr		Leu
318	<b>L</b> , 5	-1-	· · · ·	500		_, .	-1-		505					510	-7-	
	Dro	Δen	Δla		Glu	Met	Glu	Tle		Ser	Len	Tvr	Glv	Val	Glv	Tle
321	rio	Poli	515	110	OIU	MCC	Olu	520	-7-	OCI	DCu	-7-	525		011	
	Dro	Thr	-	7 ~~	λla	Тиг	T/al		Larc	T.011	Λen	Gln		Pro	Aen	Sar
			GIU	Arg	AIG	тўт	535	ıyı	цуъ	пеа	Noii	540	Der	FIO	пор	DCI
324		530	Dwa	Dho	C1 ~	т1 о			C02	71-	шia		Clu	Asp	Clu	λαn
	_	TTE	PLO	FIIE	GIII		PHE	1111	PET	AIA	555	GIU	Giu	Asp	GIU	560
	545	<b>G</b>	<b>.</b>	<b>-</b>	27.	550	77-7	Ш	7	**- 1		<b>~</b> 1	7 ~~	<b>a</b> 1	mb so	
	ser	Cys	Leu	гуѕ		GIY	vai	Tyr	ASII		Asp	GIY	Asp	Glu		vai
330	_		_	_	565	~1		<b></b>	<b>~</b>	570	<b>.</b>	7.7 -	m	3	575	T
	Pro	Val	Leu		Ата	GIY	Tyr	мет		Ala	гаг	АТА	Trp	Arg	GIY	гур
333			_•	580	_				585		_		_	590	_	<u>_</u>
335	Thr	Arg		Asn	Pro	Ser	Gly		Lys	Thr	Tyr	He		Glu	Tyr	Asn
336			595					600					605	_		
338	His	Ser	Pro	Pro	Ala	Asn	Leu	Leu	Glu	Gly	Arg		Thr	Gln	Ser	Gly
339		610					615					620				
341	Ala	His	Val	Asp	Ile	Met	Gly	Asn	Phe	Ala	Leu	Ile	Glu	Asp	Ile	Met
342	625					630					635					640
344	Arg	Val	Ala	Ala	Gly	Gly	Asn	Gly	Ser	Asp	Ile	Gly	His	Asp	Gln	Val
345					645					650					655	
347	His	Ser	Gly	Ile	Phe	Glu	Trp	Ser	Glu	Arg	Ile	Asp	Leu	Lys	Leu	
348			_	660			_		665					670		

VERIFICATION SUMMARY

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L:9 M:283 W: Missing Blank Line separator, <130> field identifier

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:10 M:283 W: Missing Blank Line separator, <160> field identifier L:12 M:283 W: Missing Blank Line separator, <210> field identifier

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